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RAW SEQUENCE LISTING

DATE: 07/28/2004

PATENT APPLICATION: US/09/545,998

TIME: 14:14:16

Input Set : N:\Crf3\RULE60\09545998.raw

Output Set: N:\CRF4\07282004\I545998.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Gorman, Daniel M.
 6 Randall, Troy D.
 7 Zlotnik, Albert

9 (ii) TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
 10 REAGENTS

12 (iii) NUMBER OF SEQUENCES: 8

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: DNAX Research Institute
 16 (B) STREET: 901 California Avenue
 17 (C) CITY: Palo Alto
 18 (D) STATE: California
 19 (E) COUNTRY: USA
 20 (F) ZIP: 94304-1104

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk
 24 (B) COMPUTER: IBM PC compatible
 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/09/545,998
 C--> 30 (B) FILING DATE: 10-Apr-2000
 W--> 35 (C) CLASSIFICATION: 536

C--> 40 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: US/08/911,423
 34 (B) FILING DATE: 14-AUG-1997
 37 (A) APPLICATION NUMBER: US 60/023,419
 38 (B) FILING DATE: 16-AUG-1996
 41 (A) APPLICATION NUMBER: US 60/027,901
 42 (B) FILING DATE: 07-OCT-1996

C--> 44 (viii) ATTORNEY/AGENT INFORMATION:

45 (A) NAME: Ching, Edwin P.
 46 (B) REGISTRATION NUMBER: 34,090
 47 (C) REFERENCE/DOCKET NUMBER: DX0612K

C--> 49 (ix) TELECOMMUNICATION INFORMATION:

50 (A) TELEPHONE: 650-852-9196
 51 (B) TELEFAX: 650-496-1200

54 (2) INFORMATION FOR SEQ ID NO: 1:

56 (i) SEQUENCE CHARACTERISTICS:

57 (A) LENGTH: 1073 base pairs
 58 (B) TYPE: nucleic acid
 59 (C) STRANDEDNESS: single

ENTERED

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60      (D) TOPOLOGY: linear
62      (ii) MOLECULE TYPE: cDNA
65      (ix) FEATURE:
66          (A) NAME/KEY: CDS
67          (B) LOCATION: 68..751
70      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
72 CTCGAGATCC ATTGTGCTGG AAAGGGAACCT CCTGAAATCA GCCGACAGAA GACTCAGGAG      60
74 AAGCACT ATG GGG GCA TGG GCC ATG CTG TAT GGA GTC TCG ATG CTC TGT      109
75      Met Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys
76      1          5          10
78 GTG CTG GAC CTA GGT CAG CCG AGT GTA GTT GAG GAG CCT GGC TGT GGC      157
79 Val Leu Asp Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly
80 15          20          25          30
82 CCT GGC AAG GTT CAG AAC GGA AGT GGC AAC AAC ACT CGC TGC TGC AGC      205
83 Pro Gly Lys Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser
84          35          40          45
86 CTG TAT GCT CCA GGC AAG GAG GAC TGT CCA AAA GAA AGG TGC ATA TGT      253
87 Leu Tyr Ala Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys
88          50          55          60
90 GTC ACA CCT GAG TAC CAC TGT GGA GAC CCT CAG TGC AAG ATC TGC AAG      301
91 Val Thr Pro Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys
92          65          70          75
94 CAC TAC CCC TGC CAA CCA GGC CAG AGG GTG GAG TCT CAA GGG GAT ATT      349
95 His Tyr Pro Cys Gln Pro Gly Gln Arg Val Glu Ser Gln Gly Asp Ile
96          80          85          90
98 GTG TTT GGC TTC CGG TGT GTT GCC TGT GCC ATG GGC ACC TTC TCC GCA      397
99 Val Phe Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala
100 95          100          105          110
102 GGT CGT GAC GGT CAC TGC AGA CTT TGG ACC AAC TGT TCT CAG TTT GGA      445
103 Gly Arg Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly
104          115          120          125
106 TTT CTC ACC ATG TTC CCT GGG AAC AAG ACC CAC AAT GCT GTG TGC ATC      493
107 Phe Leu Thr Met Phe Pro Gly Asn Lys Thr His Asn Ala Val Cys Ile
108          130          135          140
110 CCG GAG CCA CTG CCC ACT GAG CAA TAC GGC CAT TTG ACT GTC ATC TTC      541
111 Pro Glu Pro Leu Pro Thr Glu Gln Tyr Gly His Leu Thr Val Ile Phe
112          145          150          155
114 CTG GTC ATG GCT GCA TGC ATT TTC TTC CTA ACC ACA GTC CAG CTC GGC      589
115 Leu Val Met Ala Ala Cys Ile Phe Phe Leu Thr Thr Val Gln Leu Gly
116          160          165          170
118 CTG CAC ATA TGG CAG CTG AGG AGG CAA CAC ATG TGT CCC CGA GAG ACC      637
119 Leu His Ile Trp Gln Leu Arg Arg Gln His Met Cys Pro Arg Glu Thr
120 175          180          185          190
122 CAG CCA TTC GCG GAG GTG CAG TTG TCA GCT GAG GAT GCT TGC AGC TTC      685
123 Gln Pro Phe Ala Glu Val Gln Leu Ser Ala Glu Asp Ala Cys Ser Phe
124          195          200          205
126 CAG TTC CCT GAG GAG GAA CGC GGG GAG CAG ACA GAA GAA AAG TGT CAT      733
127 Gln Phe Pro Glu Glu Glu Arg Gly Glu Gln Thr Glu Glu Lys Cys His
128          210          215          220

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130 CTG GGG GGT CGG TGG CCA TGAGGCCTGG TCTTCCTCTG TGCCCCAAGC      781
131 Leu Gly Gly Arg Trp Pro
132      225
134 CAGACGCTAC AAGACTTGCC CAGCTATACC CTTGGTGAGA GCAGGGGCCA TGCTCTGCAC      841
136 CCTTCCCTGG GCCTGGCCCT GCTCCCCCTCA ACAGTGGCGG AAGTGGGTGT ATGAGAGCGG      901
138 TGAGTTACGA TTGGGCCCTA TGGCTGCCTT TCTCATTTGA CAGCTCTGTT GGAGTAGGGT      961
140 CTTTGGGCCC ACCAAGAGCA CCACGTTTAG CACAAGATCT TGTACAAGAA TAAATACTTG      1021
142 TTTAGTAACC TGAAAAAAAAA AAAAAAAGG GCGGCCGCGG AGGCCGAATT CC      1073
145 (2) INFORMATION FOR SEQ ID NO: 2:
147     (i) SEQUENCE CHARACTERISTICS:
148         (A) LENGTH: 228 amino acids
149         (B) TYPE: amino acid
150         (D) TOPOLOGY: linear
152     (ii) MOLECULE TYPE: protein
154     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
156 Met Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys Val Leu
157   1           5           10           15
159 Asp Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly Pro Gly
160           20           25           30
162 Lys Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser Leu Tyr
163           35           40           45
165 Ala Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys Val Thr
166           50           55           60
168 Pro Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys His Tyr
169   65           70           75           80
171 Pro Cys Gln Pro Gly Gln Arg Val Glu Ser Gln Gly Asp Ile Val Phe
172           85           90           95
174 Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala Gly Arg
175           100          105          110
177 Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly Phe Leu
178           115          120          125
180 Thr Met Phe Pro Gly Asn Lys Thr His Asn Ala Val Cys Ile Pro Glu
181           130          135          140
183 Pro Leu Pro Thr Glu Gln Tyr Gly His Leu Thr Val Ile Phe Leu Val
184   145          150          155          160
186 Met Ala Ala Cys Ile Phe Phe Leu Thr Thr Val Gln Leu Gly Leu His
187           165          170          175
189 Ile Trp Gln Leu Arg Arg Gln His Met Cys Pro Arg Glu Thr Gln Pro
190           180          185          190
192 Phe Ala Glu Val Gln Leu Ser Ala Glu Asp Ala Cys Ser Phe Gln Phe
193           195          200          205
195 Pro Glu Glu Glu Arg Gly Glu Gln Thr Glu Glu Lys Cys His Leu Gly
196           210          215          220
198 Gly Arg Trp Pro
199   225
201 (2) INFORMATION FOR SEQ ID NO: 3:
203     (i) SEQUENCE CHARACTERISTICS:
204         (A) LENGTH: 1006 base pairs
205         (B) TYPE: nucleic acid

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206          (C) STRANDEDNESS: single
207          (D) TOPOLOGY: linear
209          (ii) MOLECULE TYPE: cDNA
212          (ix) FEATURE:
213              (A) NAME/KEY: CDS
214              (B) LOCATION: 1..723
217          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
219 ATG GCA CAG CAC GGG GCG ATG GGC GCG TTT CGG GCC CTG TGC GGC CTG      48
220 Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu
221   1          5          10          15
223 GCG CTG CTG TGC GCG CTC AGC CTG GGT CAG CGC CCC ACC GGG GGT CCC      96
224 Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro
225          20          25          30
227 GGG TGC GGC CCT GGG CGC CTC CTG CTT GGG ACG GGA ACG GAC GCG CGC     144
228 Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg
229          35          40          45
231 TGC TGC CGG GTT CAC ACG ACG CGC TGC TGC CGC GAT TAC CCG GGC GAG     192
232 Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu
233          50          55          60
235 GAG TGC TGT TCC GAG TGG GAC TGC ATG TGT GTC CAG CCT GAA TTC CAC     240
236 Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
237   65          70          75          80
239 TGC GGA GAC CCT TGC TGC ACG ACC TGC CGG CAC CAC CCT TGT CCC CCA     288
240 Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro
241          85          90          95
243 GGC CAG GGG GTA CAG TCC CAG GGG AAA TTC AGT TTT GGC TTC CAG TGT     336
244 Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
245          100          105          110
247 ATC GAC TGT GCC TCG GGG ACC TTC TCC GGG GGC CAC GAA GGC CAC TGC     384
248 Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys
249          115          120          125
251 AAA CCT TGG ACA GAC TGC ACC CAG TTC GGG TTT CTC ACT GTG TTC CCT     432
252 Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro
253          130          135          140
255 GGG AAC AAG ACC CAC AAC GCT GTG TGC GTC CCA GGG TCC CCG CCG GCA     480
256 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala
257 145          150          155          160
259 GAG CCG CTT GGG TGG CTG ACC GTC GTC CTC CTG GCC GTG GCC GCC TGC     528
260 Glu Pro Leu Gly Trp Leu Thr Val Val Leu Ala Val Ala Ala Cys
261          165          170          175
263 GTC CTC CTC CTG ACC TCG GCC CAG CTT GGA CTG CAC ATC TGG CAG CTG     576
264 Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu
265          180          185          190
267 AGG AGT CAG TGC ATG TGG CCC CGA GAG ACC CAG CTG CTG CTG GAG GTG     624
268 Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val
269          195          200          205
271 CCG CCG TCG ACC GAA GAC GCC AGA AGC TGC CAG TTC CCC GAG GAA GAG     672
272 Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu
273          210          215          220

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275 CGG GGC GAG CGA TCG GCA GAG GAG AAG GGG CGG CTG GGA GAC CTG TGG      720
276 Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp
277 225                230                235                240
279 GTG TGAGCCTGGC CGTCCTCCGG GGCCACCGAC CGCAGCCAGC CCCTCCCCAG      773
280 Val
283 GAGCTCCCCA GGCCGCAGGG GCTCTGCGTT CTGCTCTGGG CCGGGCCCTG CTCCCCTGGC      833
285 AGCAGAAGTG GGTGCAGGAA GGTGGCAGTG ACCAGCGCCC TGGACCATGC AGTTCGGCGG      893
287 CCGCTCTAAA GGATCCAAGC TTACGTACGC GTGCATGCGA CGTCATAGCT CTTCTATAGT      953
289 GTCACCTAAA TTCAATTAC TGGCCGTCGT TTTACAACGT CCTGACTGGG AAA      1006
292 (2) INFORMATION FOR SEQ ID NO: 4:
294     (i) SEQUENCE CHARACTERISTICS:
295         (A) LENGTH: 241 amino acids
296         (B) TYPE: amino acid
297         (D) TOPOLOGY: linear
299     (ii) MOLECULE TYPE: protein
301     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
303 Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu
304 1      5      10      15
306 Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro
307      20      25      30
309 Gly Cys Gly Pro Gly Arg Leu Leu Gly Thr Gly Thr Asp Ala Arg
310      35      40      45
312 Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu
313      50      55      60
315 Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
316      65      70      75      80
318 Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro
319      85      90      95
321 Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
322      100     105     110
324 Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys
325      115     120     125
327 Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro
328      130     135     140
330 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala
331 145     150     155     160
333 Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys
334      165     170     175
336 Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu
337      180     185     190
339 Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val
340      195     200     205
342 Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu
343      210     215     220
345 Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp
346 225     230     235     240
348 Val
351 (2) INFORMATION FOR SEQ ID NO: 5:
353     (i) SEQUENCE CHARACTERISTICS:

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VERIFICATION SUMMARY

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DATE: 07/28/2004

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Input Set : N:\Crf3\RULE60\09545998.raw

Output Set: N:\CRF4\07282004\I545998.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:35 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)
L:36 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:40 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:44 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]
L:49 M:220 C: Keyword misspelled or invalid format, [(ix) TELECOMMUNICATION INFORMATION:]